

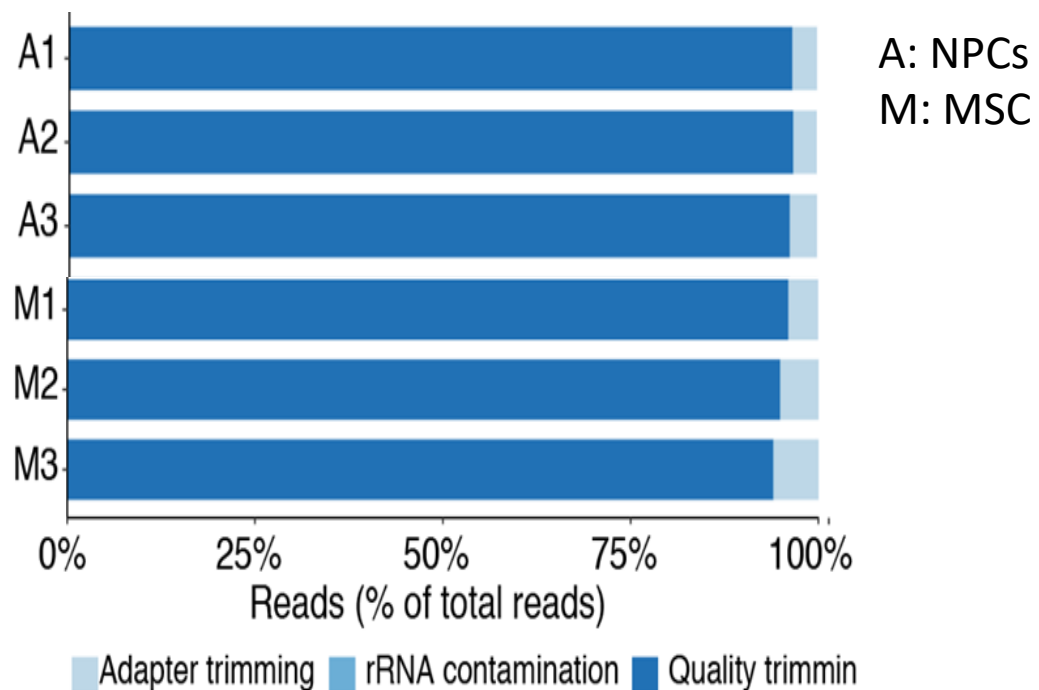
QC & MAPPING STATISTICS

The following sections provide a summary of the quality controls obtained for your dataset.

QC summary

This section includes QC and statistics after pre processing of the reads – trimming for adapters and low quality bases and removal of rRNA reads.

On an average 96% of the reads corresponding to 51.86 M reads pass the filtering criteria across all the samples.



QC statistics plot of samples

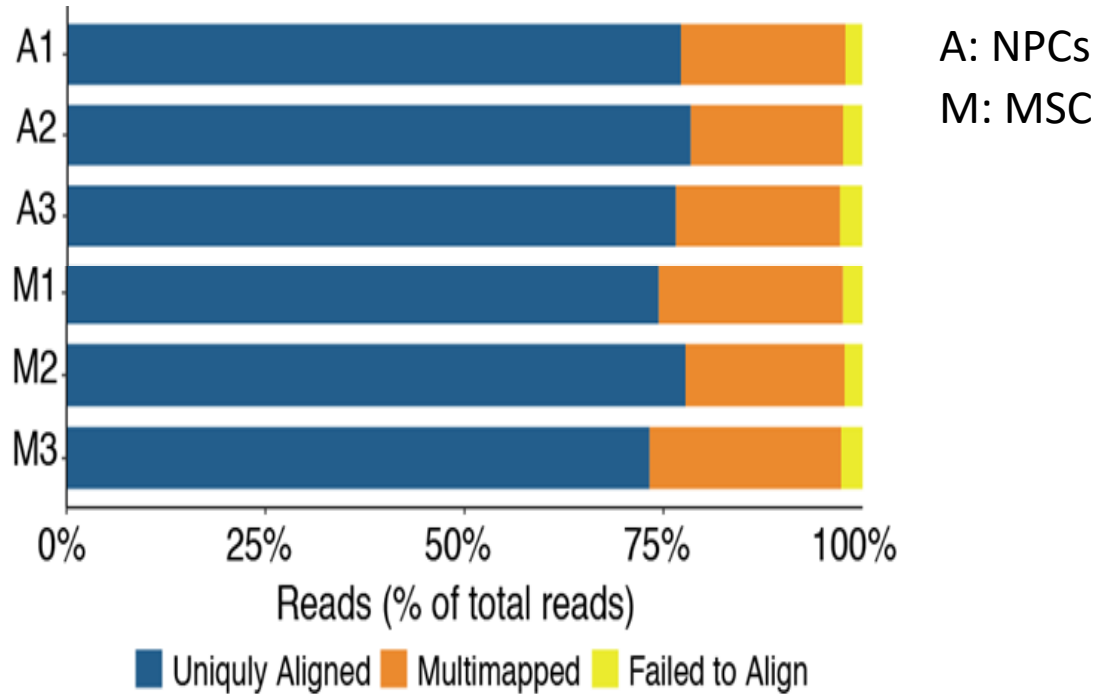
Sample	Raw reads	Adapter trimming	rRNA contamination	Quality trimming
A1	49.05	49.04	47.44	47.44
A2	47.41	47.4	45.9	45.9
A3	60.28	60.27	58.09	58.09
M1	52.15	52.12	50.04	50.04
M2	62.01	62.01	58.83	58.83
M3	52.85	52.84	49.66	49.66

QC statistics of samples. Numbers are represented in millions

Mapping Summary

This section includes the mapping statistics on the rat genome by STAR alignment tool.

On an average 97% of the reads corresponding to 50.5 M reads mapped on the genome across all the samples. (Figure 2 & Table 2)



Mapping statistics plot of samples

Sample	# Reads	Uniquely Aligned	Multi-mapped	Aligned	Failed to Align
A1	47.44	36.62	9.82	46.44	1
A2	45.9	35.98	8.82	44.8	1.1
A3	58.09	44.46	12.01	56.47	1.62
M1	50.04	37.22	11.58	48.79	1.25
M2	58.83	45.74	11.76	57.5	1.33
M3	49.66	36.37	11.96	48.32	1.34

Mapping statistics of samples. Numbers are represented in millions